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RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/875,849C

DATE: 10/01/2002

TIME: 15:07:36

Input Set: A:\LKS944A2.txt

Output Set: N:\CRF4\10012002\H875849C.raw

SEQUENCE LISTING

ENTERED

- 4 (1) GENERAL INFORMATION.
- 6 (1) APPLICANT: Briskin, Michael J.
7 Rindler, Douglas J.
8 Picarella, Dominic
9 Newman, Walter
- 11 (ii) TITLE OF INVENTION: Mucosal Vascular Addressins and Uses
12 Thereof
- 14 (iii) NUMBER OF SEQUENCES: 17
- 16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
18 (B) STREET: 530 Virginia Road, PO Box 9133
19 (C) CITY: Concord
20 (D) STATE: Massachusetts
21 (E) COUNTRY: U.S.A.
22 (F) ZIP: 01742-9133
- 24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 30 (vi) CURRENT APPLICATION DATA:
C--> 31 (A) APPLICATION NUMBER: US/08/875,849C
C--> 32 (B) FILING DATE: 08-Sep-1997
33 (C) CLASSIFICATION:
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: PCT/US96/02153
37 (B) FILING DATE: 12-FEB-1996
39 (A) APPLICATION NUMBER: US 08/523,004
41 (B) FILING DATE: 01-SEP-1995
- 43 (viii) ATTORNEY/AGENT INFORMATION:
44 (A) NAME: Brook, David E.
45 (B) REGISTRATION NUMBER: 22,592
46 (C) REFERENCE/DOCKET NUMBER: LKS94-04A2
- 48 (:x) TELECOMMUNICATION INFORMATION:
49 (A) TELEPHONE: 978-341-0036
50 (B) TELEFAX: 978-341-0136
- 52 (2) INFORMATION FOR SEQ ID NO: 1:
53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 1624 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: double
57 (D) TOPOLOGY: linear

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68	(ii) MOLECULE TYPE: cDNA	
70	(ix) FEATURE	
71	(A) NAME/KEY: CDS	
72	(B) LOCATION 1..1218	
75	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
77	AIG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTI CTG GGG CTC CTC	48
78	Met Asp Phe Gly Leu Ala Leu Leu Leu Ala Gly Leu Leu Gly Leu Leu	
79	1 5 10 15	
81	CTC GGC CAG TCC CTC CAG GTG AAG CCC CTG CAG GTG GAG CCC CCG GAG	96
82	Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Gln Pro Pro Glu	
83	20 25 30	
85	CCG GTG GTG GCC GTG GCG TIG GGN GGC TCG CGC CAG CTC ACC TGC CGC	144
86	Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg	
87	35 40 45	
89	CTG GCC TGC GCG GAC CGC GGG GCG TCG GTG CAG TGG CGG GGC CTG GAC	192
90	Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp	
91	50 55 60	
93	ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC	240
94	Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr	
95	65 70 75 80	
97	GIG CGC AAC GCC TCG CTG TCG GCG GGC ACC CGC GTG TGC GIG GGC	288
98	Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly	
99	85 90 95	
101	TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CIT GTG TAC	336
102	Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr	
103	100 105 110	
105	GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GGC CTG GTG CCT GGT	384
106	Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly	
107	115 120 125	
109	GAC CCG GAG GTG GCC IGT ACG GCC CAC AAA GTC ACG CCC GIG GAC CGC	432
110	Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro	
111	130 135 140	
113	AAC GCG CTC TCC TTC TCC CTG CTC GTC GGG GGC CAG GAA CTG GAG GGG	480
114	Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly	
115	145 150 155 160	
119	GCG CAA GCG CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG	528
120	Ala Gln Ala Leu Gly Pro Glu Val Gln Gln Glu Glu Glu Pro Gln	
121	165 170 175	
123	GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CGC	576
124	Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro	
125	180 185 190	
127	CCC CTG GGG ACC CCI GTC CCG CCC GCC CTC TAC TGC CAG GCC ACG ATG	624
128	Pro Leu Gly Thr Pro Val Pro Pro Ala Leu Tyr Cys Gln Ala Thr Met	
129	195 200 205	
131	AGG CTG CCT GGC TTG GAG CTC AGC CAC CGC CAG GGC ATC CCC GTC CTG	672
132	Ara Leu Pro Gly Leu Glu Leu Ser His Arg Gln Ala Ile Pro Val Leu	
133	210 215 220	
135	CAC AGC CCG ACC TCC CCG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT	720
136	His Ser Pro Thr Ser Pro Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro	

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137	225	230	235	240	
139	CCC AAC ACC A+C TCC CCG GAG TCT CCC GAC ACC ACC TCC CCG GAG TCT				768
140	Pro Asn Thr Thr Ser Pro Glu Ser Pro Asp Thr Thr Ser Pro Glu Ser				
141	245	250	255		
143	CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CAG GAG CCT				816
144	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Gln Glu Pro				
145	260	265	270		
147	CCC GAC ACC ACC TCC CAG GAG CCT CCC GAC ACC ACC TCC CCG GAG CCT				864
148	Pro Asp Thr Thr Ser Gln Glu Pro Pro Asp Thr Thr Ser Pro Glu Pro				
149	275	280	285		
151	CCC GAC AAG ACC TCC CCG GAG CCC GCC CCC CAG GAG GGC TCC ACA CAC				912
152	Pro Asp Lys Thr Ser Pro Gln Pro Ala Pro Gln Gln Gly Ser Inr His				
153	290	295	300		
155	ACC CCC AGG ACC CCA GGC TCC ACC AGG ACT CGC CGC CCT GAG ATC TCC				960
156	Thr Pro Arg Ser Pro Gly Ser Thr Arg Thr Arg Pro Glu Ile Ser				
157	305	310	315	320	
159	CAG GCT GGG CCC ACG CAG GGA GAA GIG ATC CCA ACA GGC TCC AAA				1008
160	Gln Ala Gly Pro Thr Gln Gly Glu Val Ile Pro Thr Gly Ser Ser Lys				
161	325	330	335		
163	CCC GCG GGT GAC CAG CTG CCC GCG GCT CTG TGG ACC AGC AGT GCG GTG				1056
164	Pro Ala Gly Asp Gln Leu Pro Ala Ala Leu Trp Thr Ser Ser Ala Val				
165	340	345	350		
167	CTG GGA CTG CTG CTC CTG GCC TTG CCC ACG TAT CAC CTC TGG AAA CGC				1104
168	Leu Gly Leu Leu Leu Ala Leu Pro Thr Tyr His Leu Trp Lys Arg				
169	355	360	365		
171	TGC CGG CAC CIG GCT GAG GAC GAC ACC CAC CCA CCA GCT TCT CTG AGG				1152
172	Cys Arg His Leu Ala Glu Asp Asp Thr His Pro Pro Ala Ser Leu Arg				
173	370	375	380		
175	CTT CTG CCC CAG GTG TCG GCC TGG GCT GGG TTA AGG GGG ACC GGC CAG				1200
176	Leu Leu Pro Gln Val Ser Ala Trp Ala Gly Leu Arg Gly Thr Gly Gln				
177	385	390	395	400	
179	GTC GGG ATC AGC CCC TCC TGAGTGCCCA GCCTTTCCCC CTGTGAAAGC				1248
180	Val Gly Ile Ser Pro Ser				
181	405				
184	AAAATAGCTT GGACCCCTTC AACTTGGAA CTGGTCAGGG CAAACCTGCC TCCCATTCTA				1308
186	CTCAAAGTCA TCCCTCTGCT CACAGAGATG GATGCATGTT CTGATTGCT CTTGGAGAA				1368
188	GCICATCAGA AACTAAAAAG AAGGCCACTG TTTCCTCAC CTACCCATGA CCTGAAGCCC				1428
190	CTCCCTGAGT GGTCCCCACC TTTCCTGAGC GAACCACGTA CTTTTACAT ACATGATTC				1488
192	ATGTCTCACG TCTCCCTAAA AATGCGTAAG ACCAAGCTGT GCCCTGACCA CCCTGGGCC				1548
194	CTGTCGTCA GACCTCTGA GGCTTTGGCA AATAAACCTC CTAAAATGAT AAAAAAAA				1608
196	AAAAAAAAA AAAAAA				1624
199	(2) INFORMATION FOR SEQ ID NO: 2:				
201	(i) SEQUENCE CHARACTERISTICS:				
202	(A) LENGTH: 406 amino acids				
203	(B) TYPE: amino acid				
204	(D) TOPOLOGY: linear				
206	(ii) MOLECULE TYPE: protein				
209	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:				
211	Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu				

RAW SEQUENCE LISTING

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Input Set : A:\LKS944A2.txt

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212	1	5	10	15													
213	Leu	Gly	Gln	Ser	Leu	Gln	Val	Lys	Pro	Leu	Gln	Val	Glu	Pro	Pro	Glu	
214																	
215																	
216																	
217	20							25									30
218	Pro	Val	Val	Ala	Val	Ala	Leu	Gly	Ala	Ser	Arg	Gln	Leu	Thr	Cys	Arg	
219																	
220																	
221	35							40									45
222	Leu	Ala	Cys	Ala	Asp	Arg	Gly	Ala	Ser	Val	Gln	Trp	Arg	Gly	Leu	Asp	
223																	
224	50							55									60
225	Thr	Ser	Leu	Gly	Ala	Val	Gln	Ser	Asp	Ihr	Gly	Arg	Ser	Val	Leu	Thr	
226																	
227	65							70									80
228	Val	Arg	Asn	Ala	Ser	Leu	Ser	Ala	Ala	Gly	Thr	Arg	Val	Cys	Val	Gly	
229																	
230	85							90									95
231	Ser	Cys	Gly	Gly	Arg	Thr	Phe	Gln	His	Thr	Val	Gln	Leu	Leu	Val	Tyr	
232																	
233	100							105									110
234	Ala	Phe	Pro	Asp	Gln	Leu	Ihr	Val	Ser	Pro	Ala	Ala	Leu	Val	Pro	Gly	
235																	
236	115							120									125
237	Asp	Pro	Glu	Val	Ala	Cys	Ihr	Ala	His	Lys	Val	Thr	Pro	Val	Asp	Pro	
238																	
239	130							135									140
240	Asn	Ala	Leu	Ser	Phe	Ser	Leu	Leu	Val	Gly	Gly	Gln	Glu	Leu	Glu	Gly	
241																	
242	145							150									160
243	Ala	Gln	Ala	Leu	Gly	Pro	Glu	Val	Gln	Glu	Glu	Glu	Glu	Pro	Gln		
244																	
245	165							170									175
246	Gly	Asp	Glu	Asp	Val	Leu	Phe	Arg	Val	Thr	Glu	Arg	Trp	Arg	Leu	Pro	
247																	
248	180							185									190
249	Pro	Leu	Gly	Thr	Pro	Val	Pro	Pro	Ala	Leu	Tyr	Cys	Gln	Ala	Thr	Met	
250																	
251	195							200									205
252	Arg	Leu	Pro	Gly	Leu	Glu	Leu	Ser	His	Arg	Gln	Ala	Ile	Pro	Val	Leu	
253																	
254	210							215									220
255	His	Ser	Pro	Thr	Ser	Pro	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Pro	
256																	
257	225							230									240
258	Pro	Asn	Thr	Thr	Ser	Pro	Glu	Ser	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Ser	
259																	
260	245							250									255
261	Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	
262																	
263	260							265									270
264	Pro	Asp	Thr	Thr	Ser	Gln	Glu	Pro	Pro	Asp	Thr	Thr	Ser	Pro	Glu	Pro	
265																	
266	275							280									285
267	Arg	Leu	Pro	Gly	Leu	Glu	Pro	Ala	Pro	Gln	Gly	Ser	Thr	His			
268																	
269	290							295									300
270	Thr	Pro	Arg	Ser	Pro	Gly	Ser	Thr	Arg	Thr	Arg	Arg	Pro	Glu	Ile	Ser	
271																	
272	305							310									320
273	Gln	Ala	Gly	Pro	Thr	Gln	Gly	Glu	Val	Ile	Pro	Thr	Gly	Ser	Ser	Lys	
274																	
275	325							330									335
276	Pro	Ala	Gly	Asp	Gln	Leu	Pro	Ala	Ala	Ile	Trp	Thr	Ser	Ser	Ala	Val	
277																	
278	340							345									350
279	Leu	Gly	Leu	Leu	Leu	Ala	Leu	Pro	Thr	Tyr	His	Leu	Trp	Lys	Arg		
280																	
281	355							360									365
282	Cys	Arg	His	Leu	Ala	Glu	Asp	Asp	Thr	His	Pro	Pro	Ala	Ser	Leu	Arg	
283																	
284	370							375									380
285	Leu	Leu	Pro	Gln	Val	Ser	Ala	Trp	Ala	Gly	Leu	Arg	Gly	Thr	Gly	Gln	
286																	
287	385							390									395
288																	400

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286 Val Gly Ile Ser Pro Ser
287 405

290 (2) INFORMATION FOR SEQ ID NO: 3:

292 (i) SEQUENCE CHARACTERISTICS:

293 (A) LENGTH: 1539 base pairs

294 (B) TYPE: nucleic acid

295 (C) STRANDEDNESS: double

296 (D) TOPOLOGY: linear

298 (ii) MOLECULE TYPE: cDNA

300 (ix) FEATURE:

301 (A) NAME/KEY: CDS

302 (B) LOCATION: 1..1146

306 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

308 ATG GAT TTC GGA CTG GCC CTC CTG CTG GCG GGG CTT CTG CGG CTC CTC 48

309 Met Asp Phe Gly Leu Ala Leu Leu Ala Gly Leu Leu Gly Leu Leu

310 1 5 10 15

312 CTC GGC CAG TCC CTC CAG GTG AAG CCG CTG CAG GTG GAG CCC CCC GAG 96

313 Leu Gly Gln Ser Leu Gln Val Lys Pro Leu Gln Val Glu Pro Pro Glu

314 20 25 30

316 CCG GTG GTG GCC GTG GCC TTG GGC GCC TCG CGC CAG CTC ACC TGC CGC 144

317 Pro Val Val Ala Val Ala Leu Gly Ala Ser Arg Gln Leu Thr Cys Arg

318 35 40 45

320 CTG GCC TGC GCG GAC CGC GGG GCC TCG GTG CAG TGG CGG GGC CTG GAC 192

321 Leu Ala Cys Ala Asp Arg Gly Ala Ser Val Gln Trp Arg Gly Leu Asp

322 50 55 60

324 ACC AGC CTG GGC GCG GTG CAG TCG GAC ACG GGC CGC AGC GTC CTC ACC 240

325 Thr Ser Leu Gly Ala Val Gln Ser Asp Thr Gly Arg Ser Val Leu Thr

326 65 70 75 80

328 GTG CGC AAC GCC TCG CTG TCG GCG GCC GGG ACC CGC GTG TGC GTG GGC 288

329 Val Arg Asn Ala Ser Leu Ser Ala Ala Gly Thr Arg Val Cys Val Gly

330 85 90 95

332 TCC TGC GGG GGC CGC ACC TTC CAG CAC ACC GTG CAG CTC CTT GTG TAC 336

333 Ser Cys Gly Gly Arg Thr Phe Gln His Thr Val Gln Leu Leu Val Tyr

334 100 105 110

336 GCC TTC CCG GAC CAG CTG ACC GTC TCC CCA GCA GCC CTG GTG CCT GGT 384

337 Ala Phe Pro Asp Gln Leu Thr Val Ser Pro Ala Ala Leu Val Pro Gly

338 115 120 125

340 GAC CCG GAG GTG GCC TGT ACG GCG CAC AAA GTC ACG CCC GTG GAC CCC 432

341 Asp Pro Glu Val Ala Cys Thr Ala His Lys Val Thr Pro Val Asp Pro

342 130 135 140

344 AAC GCG CTC TCC TTC CTC GTC GCG GGG CAG GAA CTG GAG GGG 480

345 Asn Ala Leu Ser Phe Ser Leu Leu Val Gly Gly Gln Glu Leu Glu Gly

346 145 150 155 160

348 GCG CAA GCC CTG GGC CCG GAG GTG CAG GAG GAG GAG GAG CCC CAG 528

349 Ala Gln Ala Leu Gly Pro Glu Val Gln Glu Glu Glu Glu Pro Gln

350 165 170 175

352 GGG GAC GAG GAC GTG CTG TTC AGG GTG ACA GAG CGC TGG CGG CTG CCG 576

353 Gly Asp Glu Asp Val Leu Phe Arg Val Thr Glu Arg Trp Arg Leu Pro

354 180 185 190